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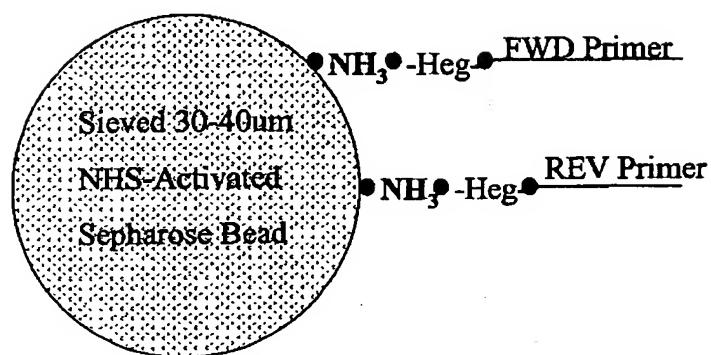
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FIGURE 1

A



B



C

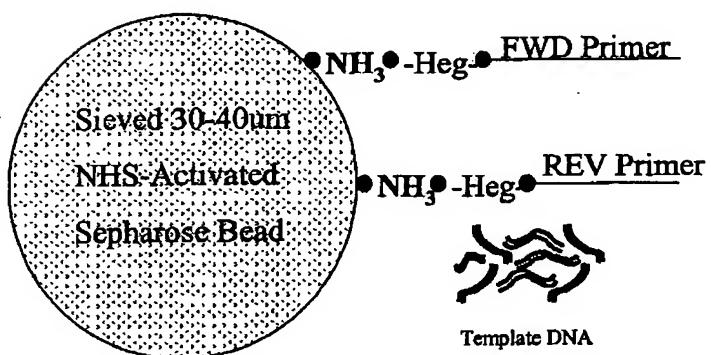
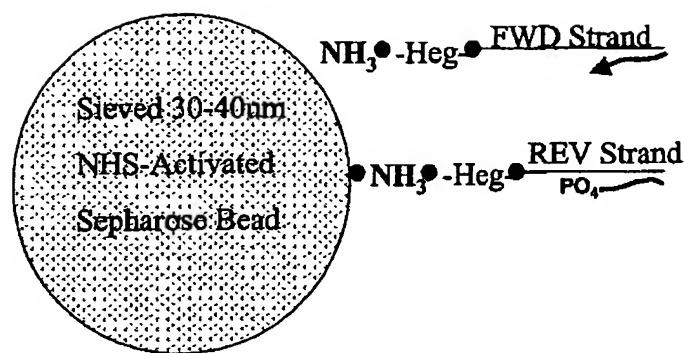
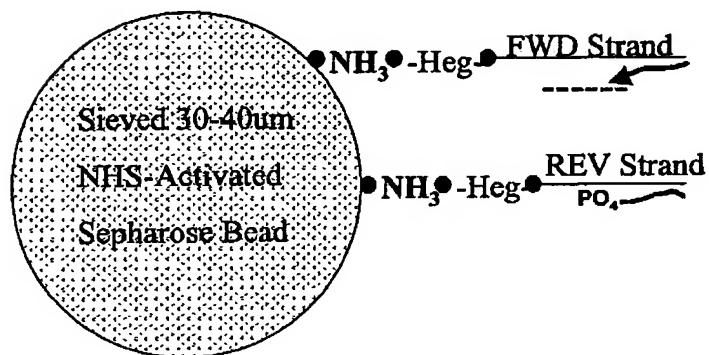


FIGURE 1

D



E



F

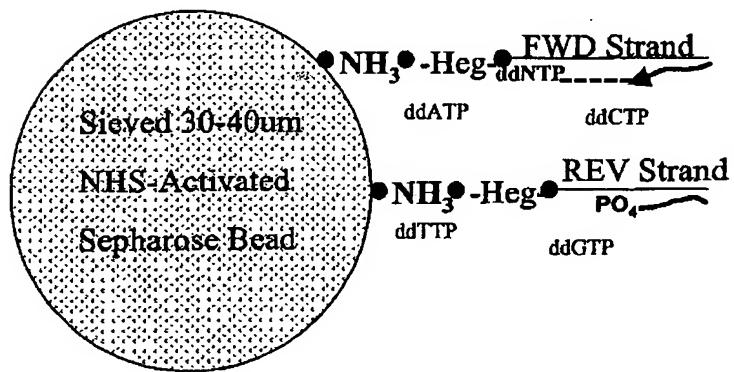
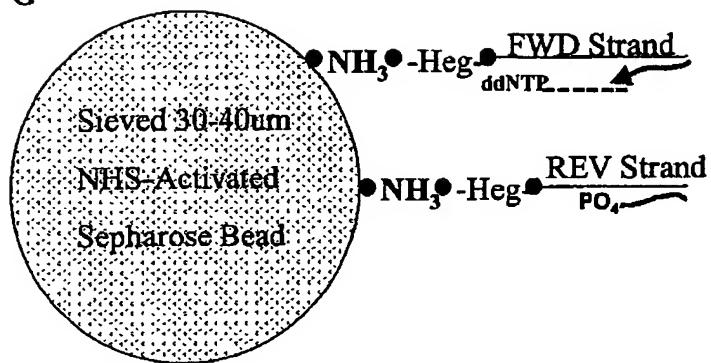
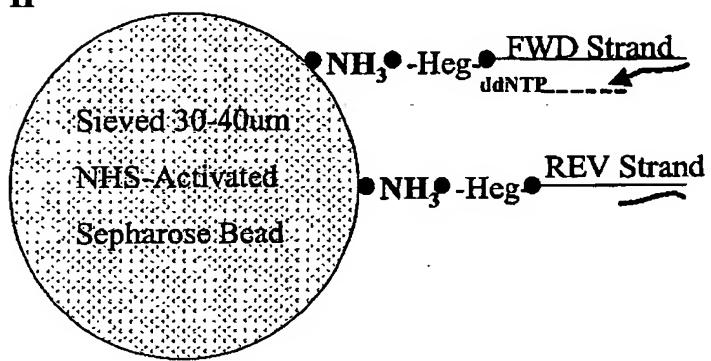


FIGURE 1

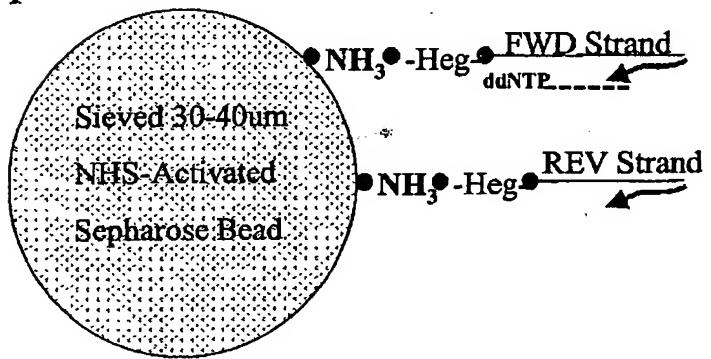
G



H



I



J

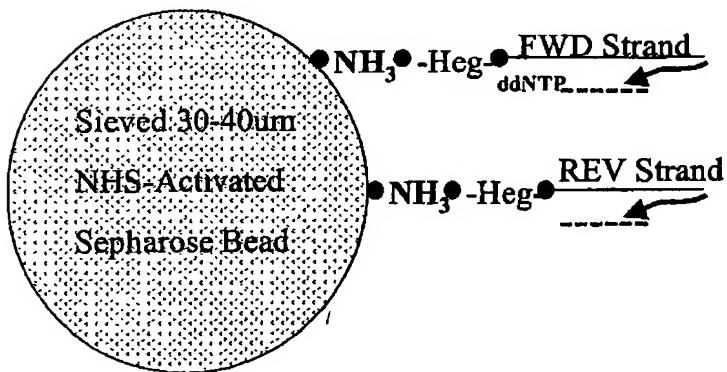


FIGURE 2

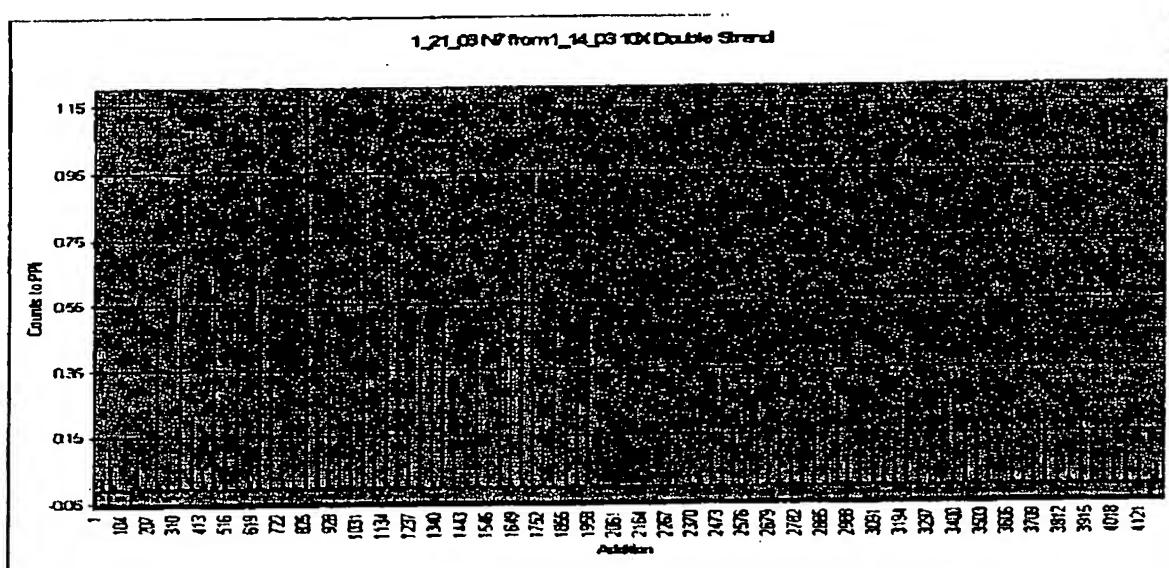
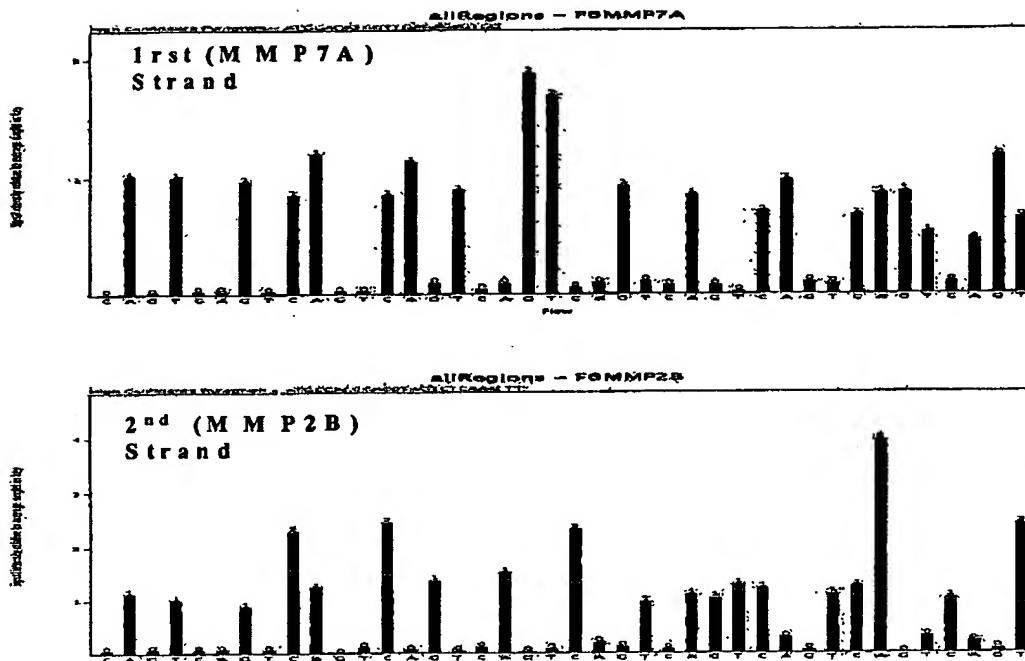


FIGURE 3

A)



Sample	Well Location	Sequence	Perfect Match Length
1st Strand (MMP7A)	F6_14_1 00001_1362_1660.well	ATGCACATGGTTGACACAGTGTT	22

ATGC ACATGGTTGACACAGTGG

ATGC CACCGACCTAGTCCTCAAACTT

Sample	Well Location	Sequence	Perfect Match Length
2nd Strand (MMP2B)	F6_14_1 00003_1363_1660.well	ATGCCACCGACCTAGTCTCAAACCTT	25

FIGURE 4

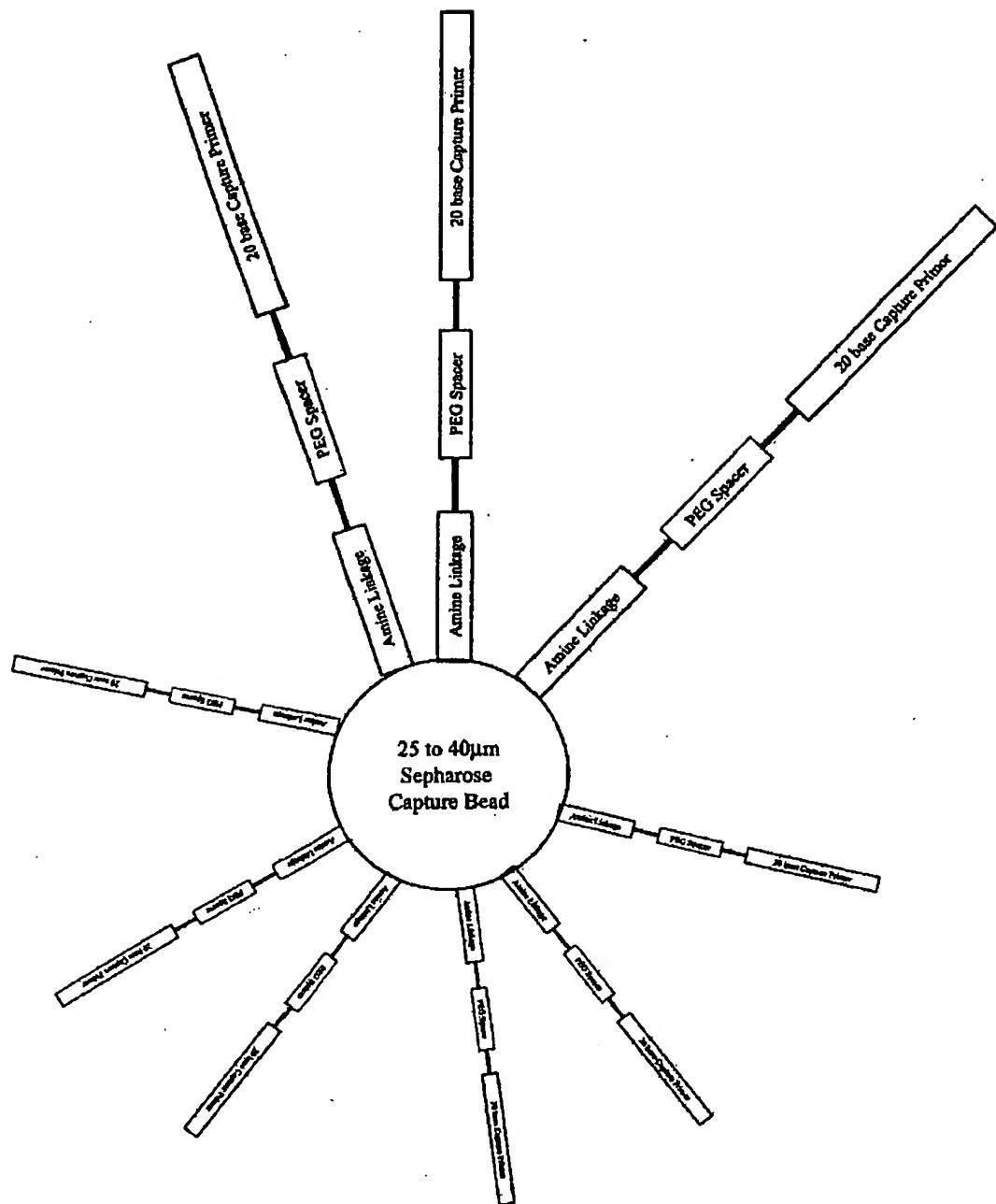


Fig. 5

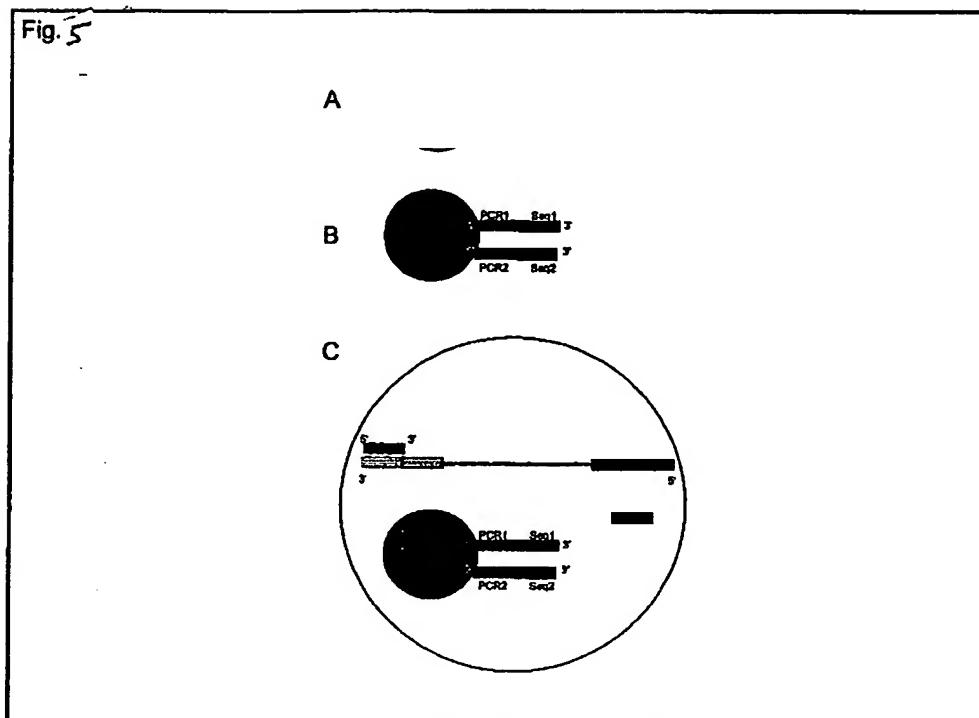


Fig. 6

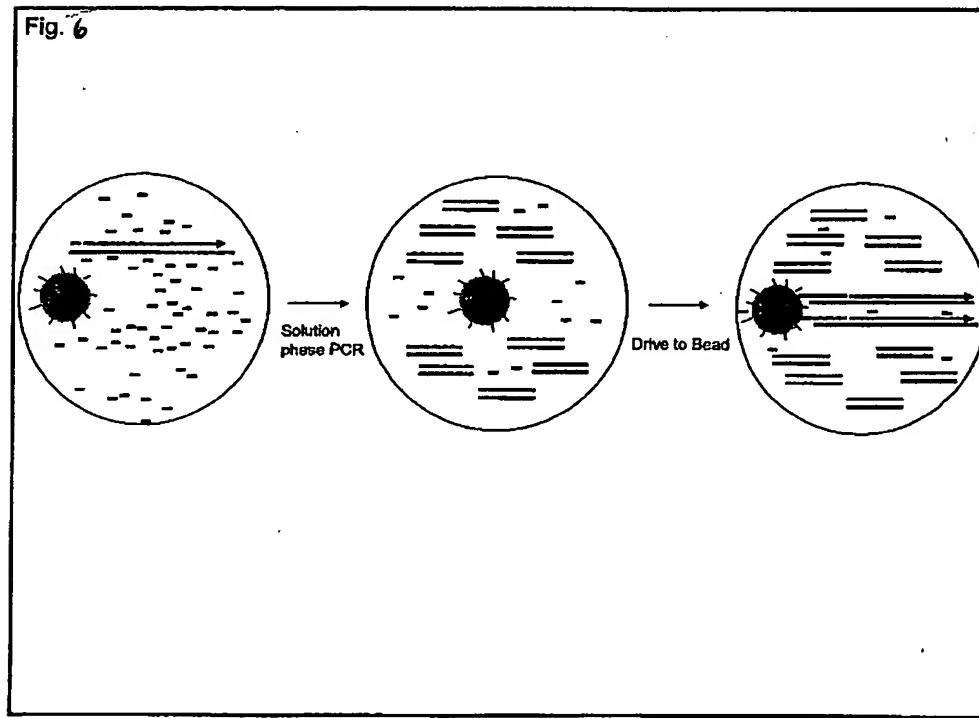


Fig. 7

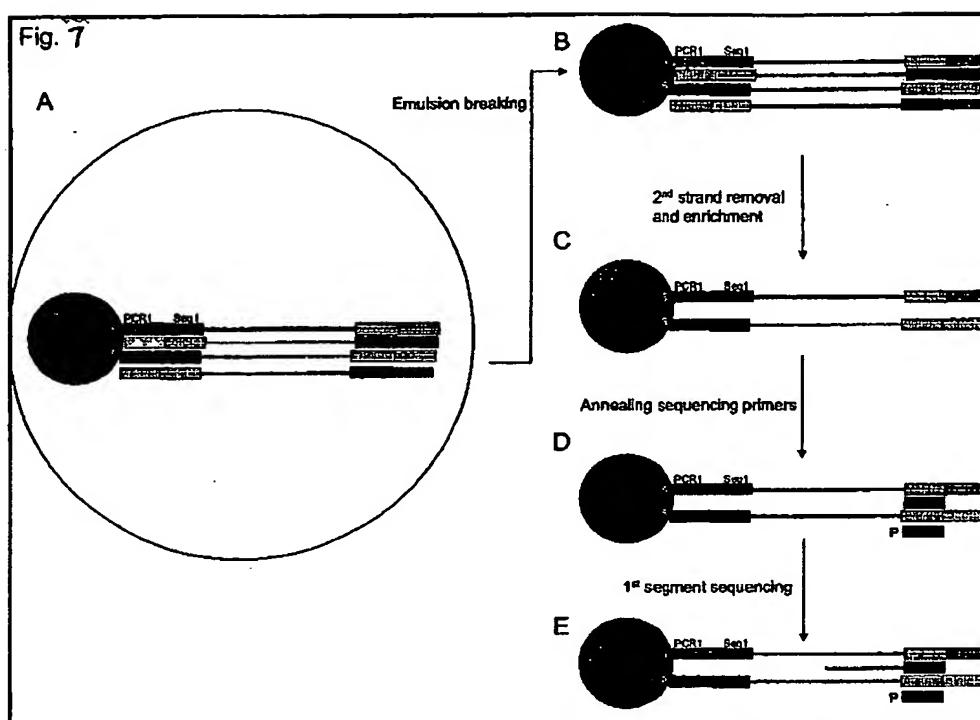


Fig. 8

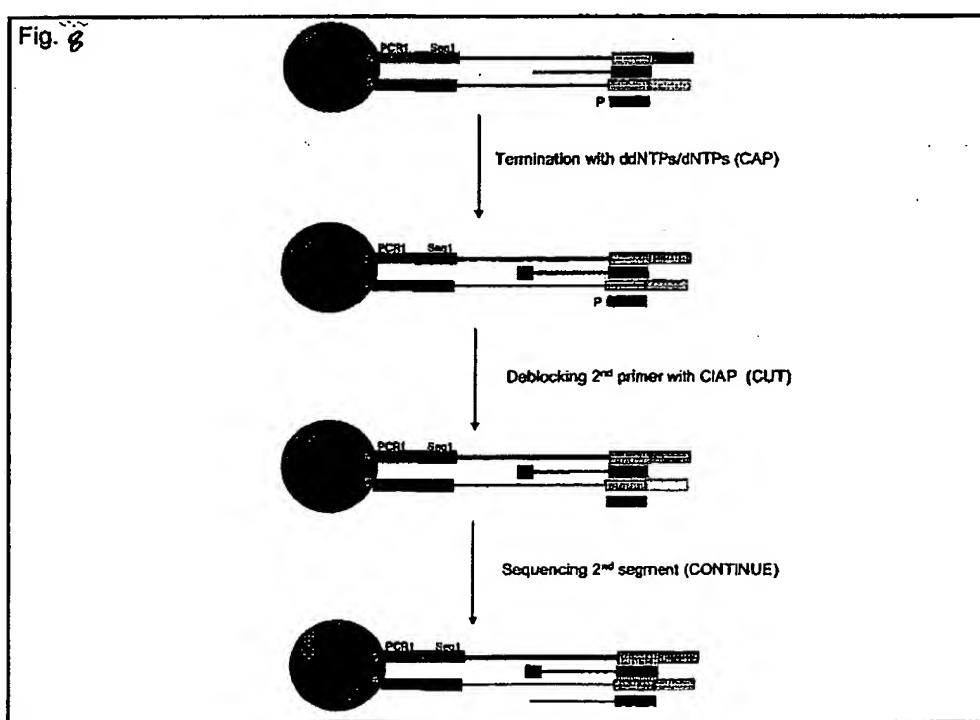
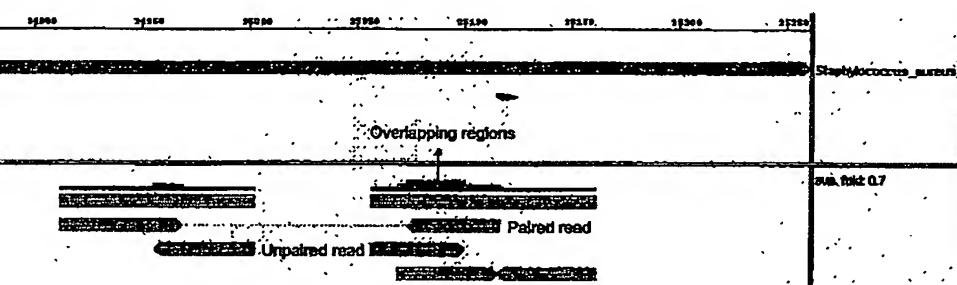


Fig. 9

A



B

Total Reads	31,785
Total 1st Strand	15,770
Total 2nd strand	16,015
Paired	11,799
Non Paired Reads	8,187
Total Coverage	38%

Fig. 10

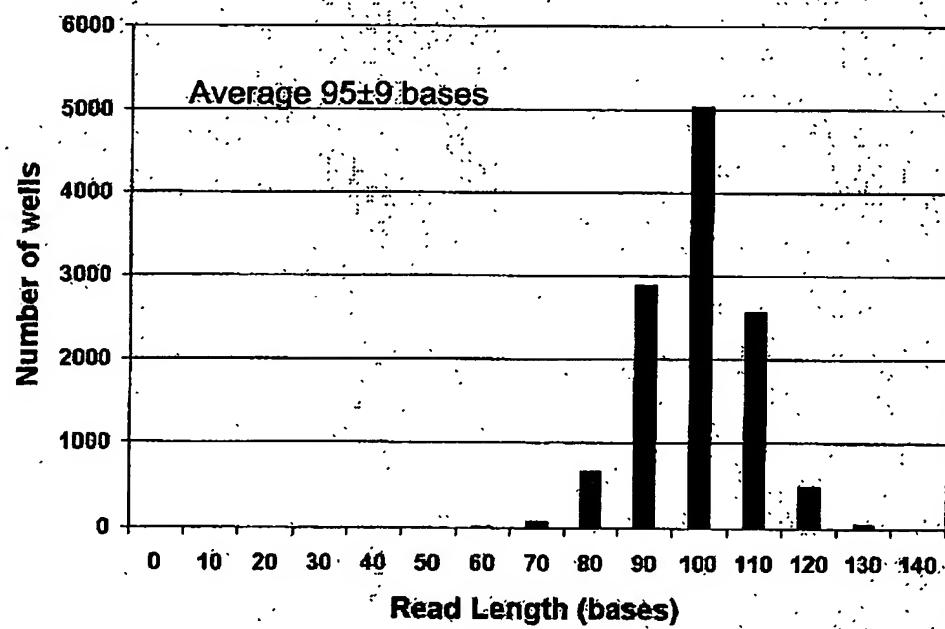


Fig. II

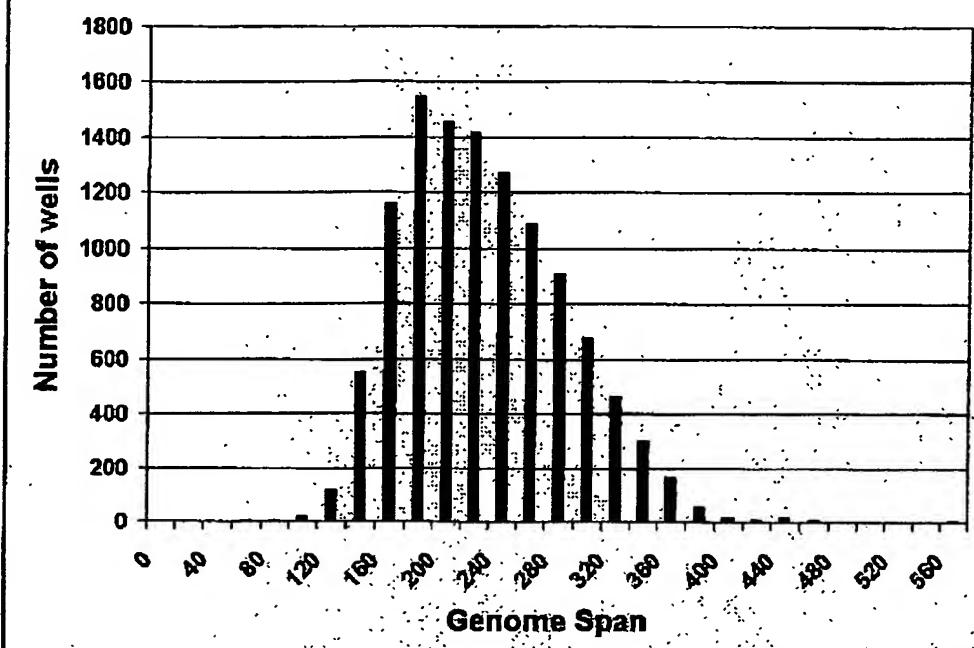


Fig. 12

Well	Genome Position	Orientation	Alignment String
00364 0548 2609	571366	F	TATTTGTGATGCTGTAAAGAAGCTACTGGTGTAGATTATGAAAGTT
00384 0548 2509 D2	571512	R	TGCTCAAAGAATTCAATTAAAATGACCATAATTCAATTATCTT
01383 0386 2232	1487690	R	AAAGCAGAACAGTCAGTACCCACAGTCAGTGACITTAACACAAGCGGAT
00383 0865 2232 D2	1487769	F	TACAGGTGTTGGTATGCCATTGGCATTGGTGCCTTGGTAGCCG
00397 0340 2923	2611033	F	AAACATATAAAACATCCCCATATCTCAATTCCSCTTCCCATGTAAACAAAAAAAGC
00397 0340 2923 D2	2611164	R	TAGATATCACTTGGCTGTTACTGGTAATGCAGGCATGAG
00417 0811 1933	122001	R	ATTCGAACCTCTGGAAATGCTTCTGATAACGGCTEGATGATG
00417 0611 1933 D2	121930	F	GATGAGGGAGCTGCAATGGCAATGGGTTAAAGGCATCATCG
00434 0696 0993	2022591	R	TGTATCTGATTGGATTAGTTCGCTTTGCACTCTTCAATTAGACC
00434 0595 0993 D2	2022473	F	CATTAACATCTGCACCGAGAAATAGCTTCTAAATACGATTGC
00443 1003 0754	107373	F	GCBACCGACGTCAGCTAATAACBCTGCACTTAAGGCTAATGATAAT
00443 1003 0754 D2	107302	R	AAACCATGCAAGATGCTAACAAAGCTCAASCATTACCAAGAACT
00454 1257 3047	59038	R	TGTTGCTGCATCATATAATTAACTACATCATCATTAATCTTGG
00454 1257 3047 D2	590860	F	GCAGATGGTGTGACTAACCAAGTTGGTAAAGTGCCTAAATAACAAAAGAT